Predicting Protein Levels In Cells

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Overview

- Data from TCGA network (http://cancergenome.nih.gov)
- Linear Regression
- Support vector regression, kernels
- Feature selection
- Gene data
- Datasets

Linear Regression (Rawlings, 1998)

- Fit a linear model to the data
- $y = X\beta + \epsilon$
- Minimise residual sum of squares between predicted and observed dependent variable

Support Vector Regression (Smola, 2004)

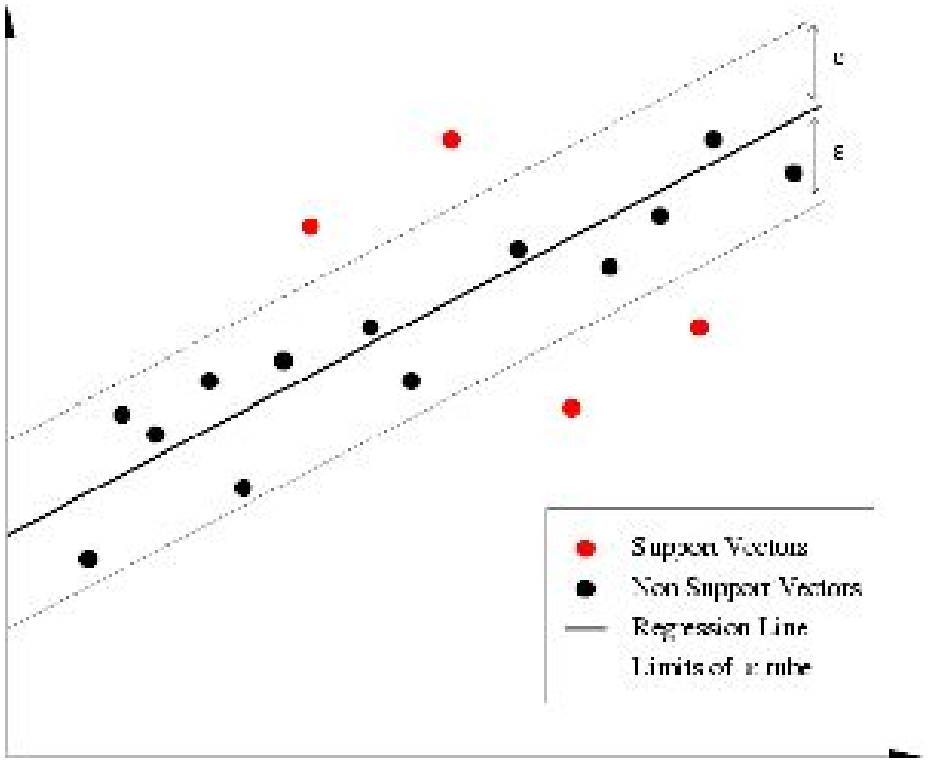


Figure 1: SVR (Gilardi, 2001)

Kernel trick

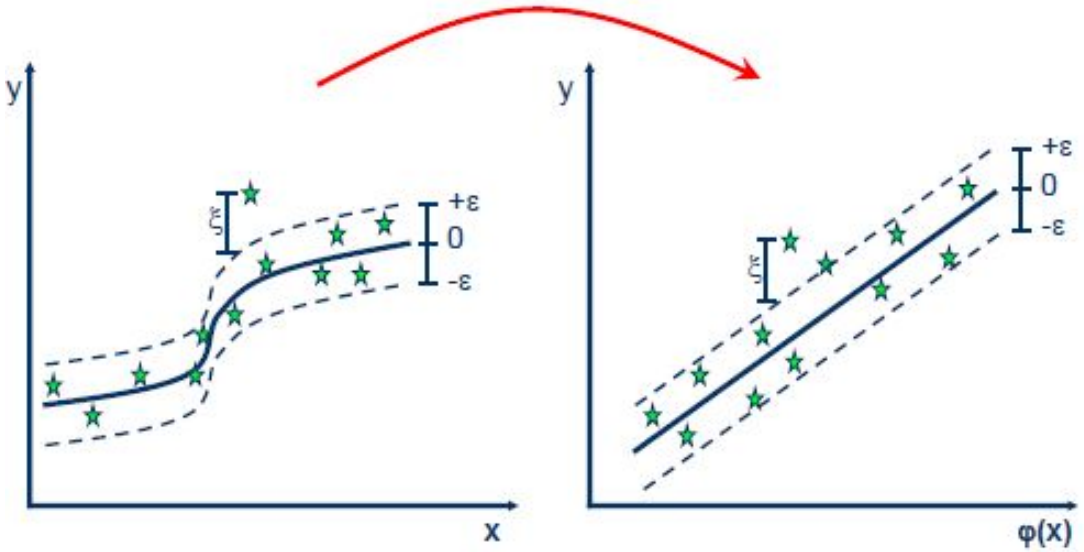
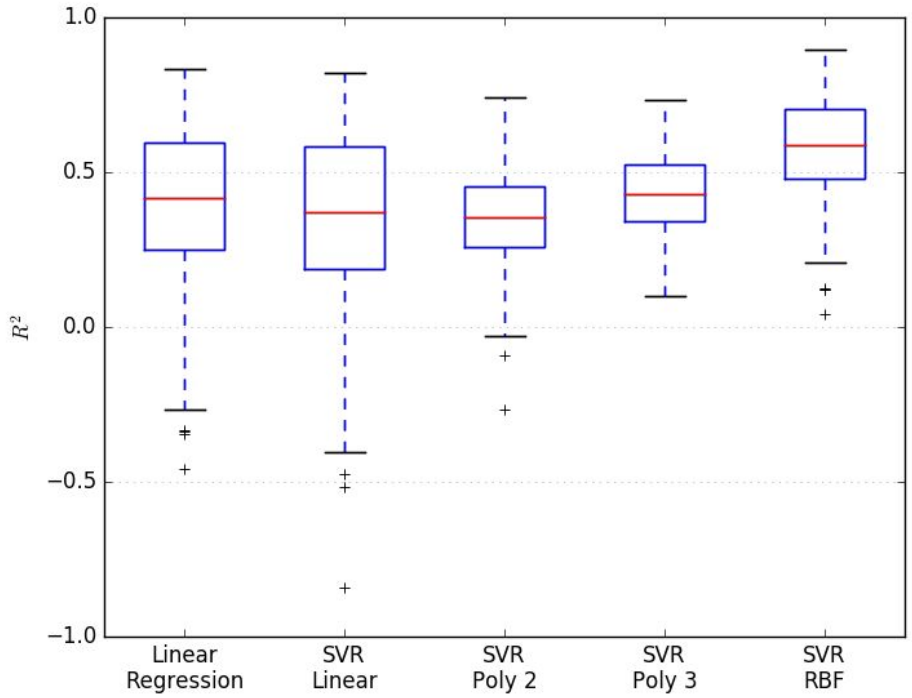


Figure 2: Kernel trick (Sayad, 2016)

Kernels:

- Linear
- Polynomial
- Radial basis function (RBF)

Results: LR vs SVR



Method	Mean R^2
Lin. Reg.	0.398
SVR Linear	0.346
SVR Poly 2nd	0.354
SVR Poly 3rd	0.430
SVR RBF	0.577

Feature selection

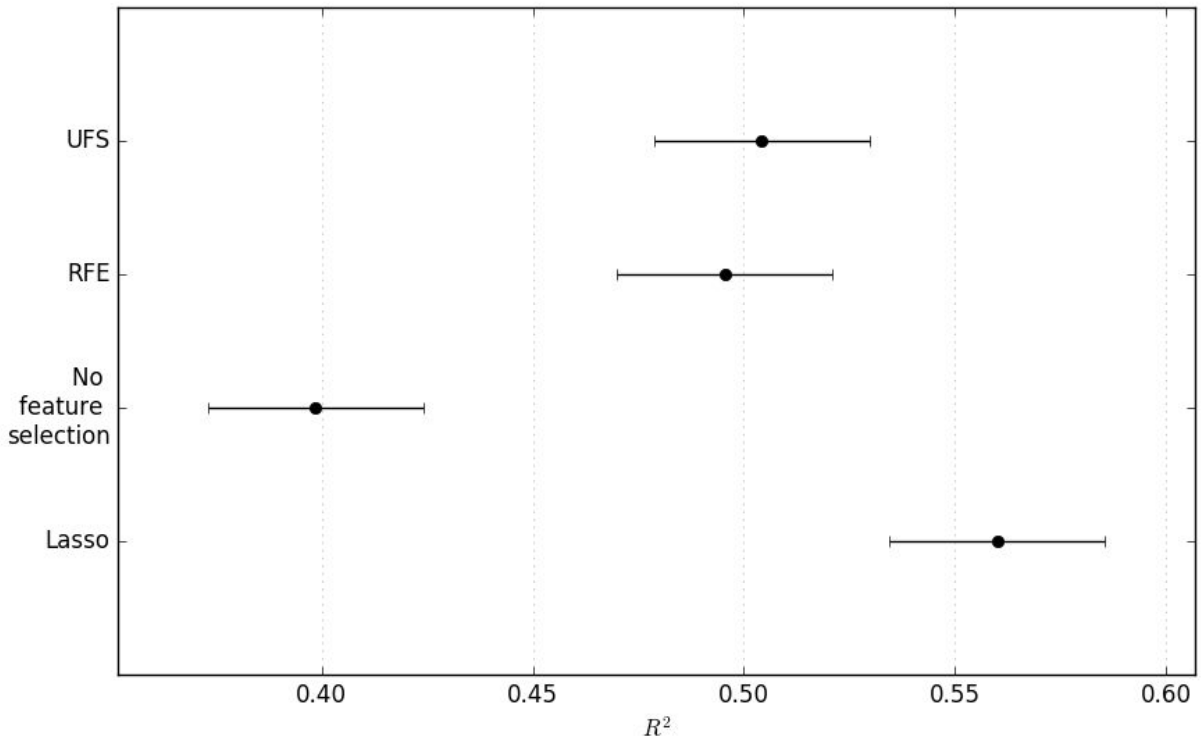
- Univariate feature selection (UFS)

  → f-test (Zhang, 1997)

- Recursive feature elimination (RFE) (Guyon, 2002)

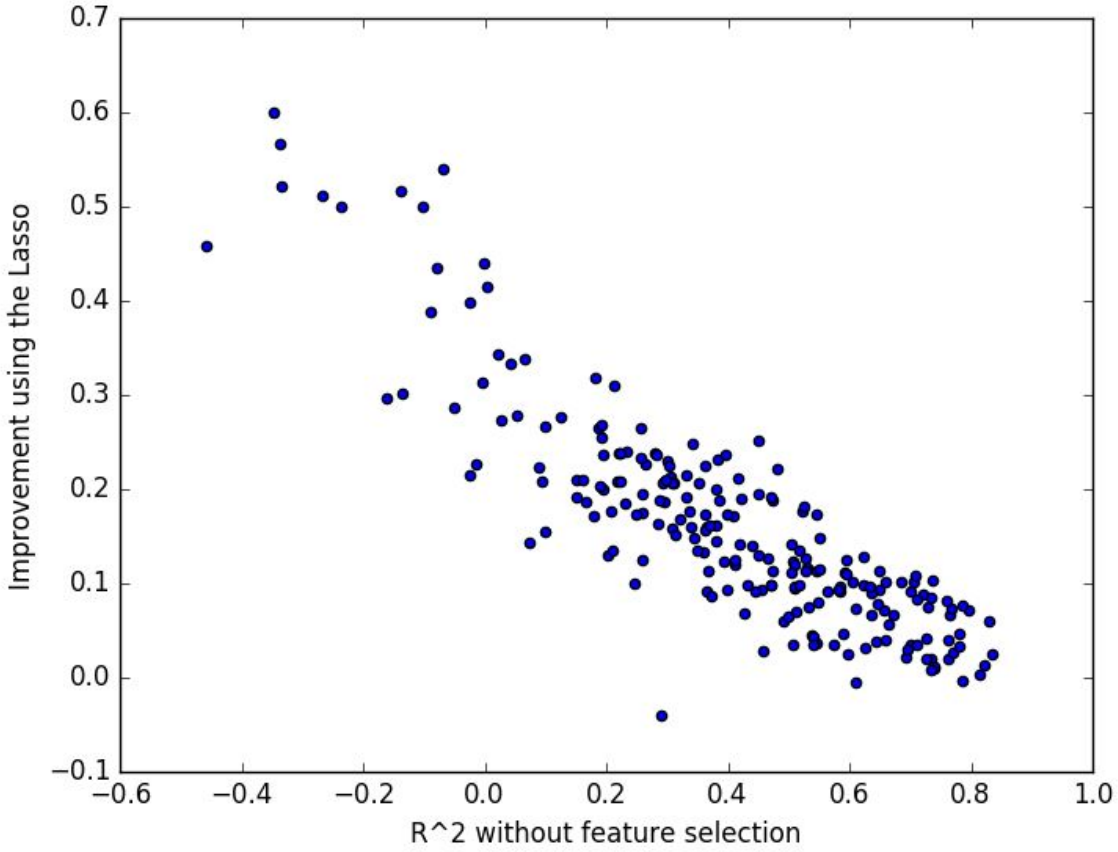
- The Lasso (Tibshirani, 1996)

Results: feature selection

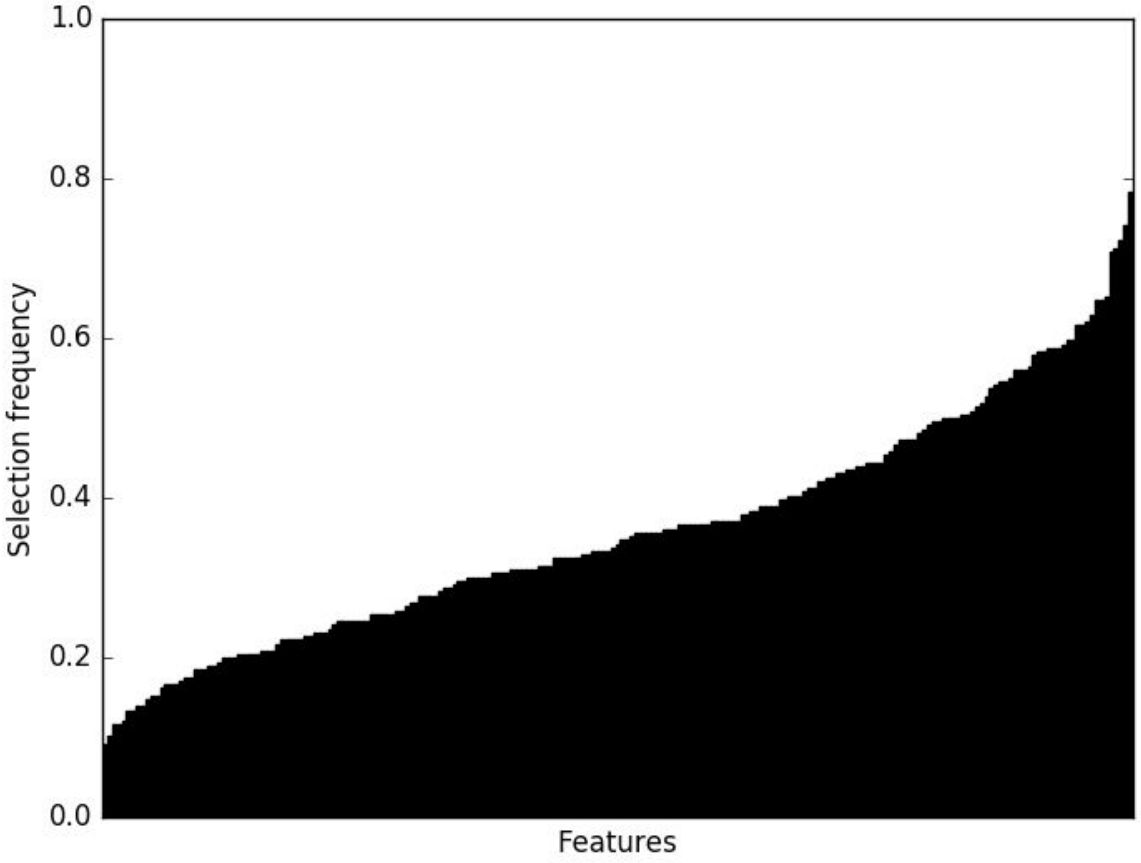


	SVR RBF	LR with Lasso
Mean R^2	0.577	0.560

Which proteins benefit the most?



Are some proteins generally more useful?



Including gene data

- Including all available gene data overwhelms algorithms
- **Approach A**: Proteins have one or more genes which code for them

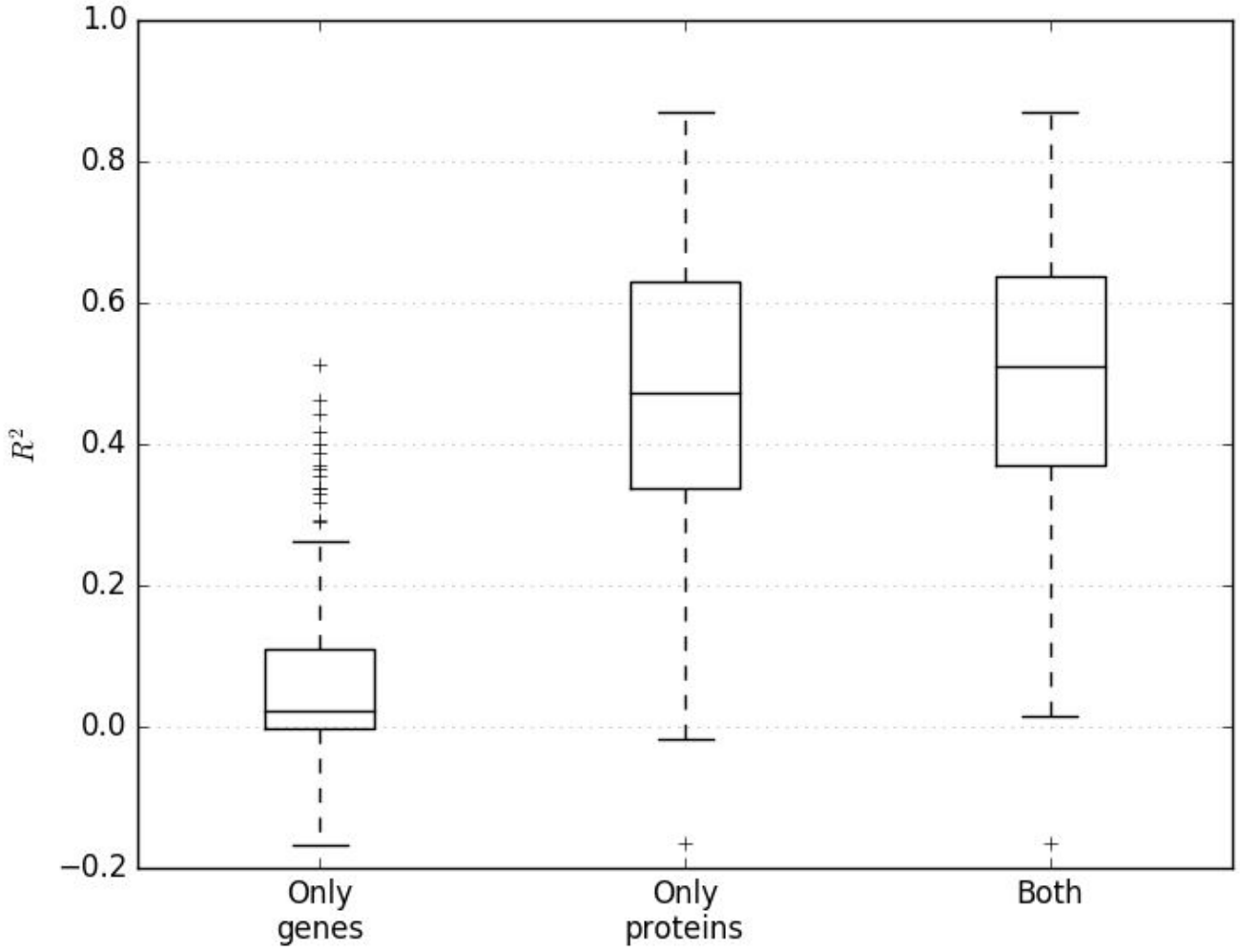
  → Use only coding genes

- **Approach B**: Genes can be grouped in pathways, in which genes interact

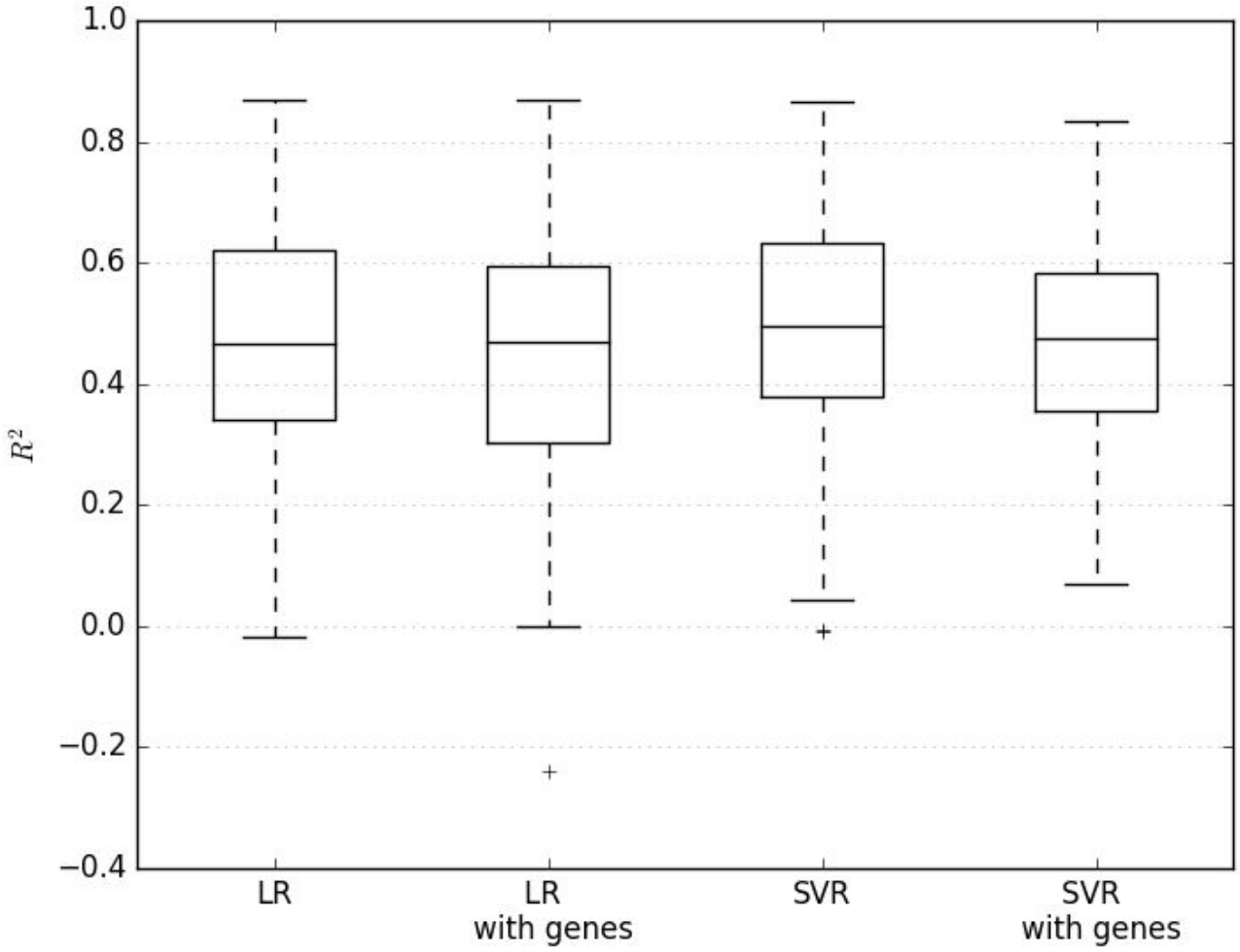
  →Use all genes from all pathways which include

  coding gene

Approach A: Coding genes (SVR)



Approach B: Pathway genes



Conclusion

- SVR with RBF kernel most useful
- Feature selection improves Linear regression performance
- Gene data not very useful.

Reference list

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